

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Problem Image Mailbox.**

# SEQUENCE LISTING

<110> J. Turck  
 J. Archer  
  
 <120> CONTROL OF GENE EXPRESSION IN EUKARYOTES  
  
 <130> 9341-021  
  
 <140> To be assigned  
 <141> 1999-12-22  
  
 <150> UK 9828660.2  
 <151> 1998-12-24  
  
 <160> 19  
  
 <170> PatentIn Ver. 2.1  
  
 <210> 1  
 <211> 7599  
 <212> DNA  
 <213> Rhodococcus sp.  
  
 <220>  
 <221> CDS  
 <222> (295)..(1035)  
 <223> ohpR regulator  
  
 <220>  
 <221> CDS  
 <222> (1261)..(2805)  
 <223> ohpA transport  
  
 <220>  
 <221> CDS  
 <222> (2807)..(4720)  
 <223> ohpB monooxygenase  
  
 <220>  
 <221> CDS  
 <222> (5721)..(6665)  
 <223> ohpD catechol 2,3-dioxygenase  
  
 <220>  
 <221> CDS  
 <222> ()...  
  
 <400> 1  
 gaattccatg ttctttctcct tgcattgtggc ccgcgttgcc gagggcactg 50  
 g ctgcggcctgt cgcccgcgaga gggcgcatgt ccgggtgcct ggatatggcg 101  
 cgtacggcgt gccctccggc gttaaccccg aggttggcca cgatgccccg gccatcaggt 161  
 ctggaatgct agcgttccag acgaaggtaa cccacagtga ctcacaccac aagtactaga 221

atgcaagctg ttgcggtgag cgccgcggca taagggggag ccatgtccgg gacgccgacg 281  
 gaaagcctga ctcg atg acc acc acc gac acc ggc ccc aag ccg ggc agt 331  
                     Met Thr Thr Thr Asp Thr Gly Pro Lys Pro Gly Ser  
                     1                    5                    10  
  
 gag gcc gcc gcc ctg ctc gcc aat gtc cgc acc tcg ggg gcg cgg ctg 379  
 Glu Ala Ala Ala Leu Leu-Ala Asn Val Arg Thr Ser Gly Ala Arg Leu  
                     15                    20                    25  
  
 tcc tcc gcg ttg tac gac att ctg aag aac cgg ctg ctc gaa ggg cgc 427  
 Ser Ser Ala Leu Tyr Asp Ile Leu Lys Asn Arg Leu Leu Glu Gly Arg  
                     30                    35                    40  
  
 tat gcg gca ggc gag aag atc gtc gtc gag tcg atc cgg caa gag ttc 475  
 Tyr Ala Ala Gly Glu Lys Ile Val Val Glu Ser Ile Arg Gln Glu Phe  
                     45                    50                    55                    60  
  
 ggg gtg agc aag cag ccc gtc atg gac gct ctg cgc cgc ctg tcc agc 523  
 Gly Val Ser Lys Gln Pro Val Met Asp Ala Leu Arg Arg Leu Ser Ser  
                     65                    70                    75  
  
 gac aag ctg gtc cac atc gtt ccc cag gtc ggt tgc gag gtc gtc tcc 571  
 Asp Lys Leu Val His Ile Val Pro Gln Val Gly Cys Glu Val Val Ser  
                     80                    85                    90  
  
 tac gcc ccg cgc gaa gtg gaa gac ttc tac acc ctg ttc ggc ggt ttc 619  
 Tyr Ala Pro Arg Glu Val Glu Asp Phe Tyr Thr Leu Phe Gly Gly Phe  
                     95                    100                    105  
  
 gaa ggg acc atc gcc gcg gta gcg gcc tcc cgg cgg acc gag gcc cag 667  
 Glu Gly Thr Ile Ala Ala Val Ala Ala Ser Arg Arg Thr Glu Ala Gln  
                     110                    115                    120  
  
 ttg ctg gag ctg gac ctg atc tcg gcg cgg gtc gac gcc ctg atc acc 715  
 Leu Leu Glu Leu Asp Leu Ile Ser Ala Arg Val Asp Ala Leu Ile Thr  
                     125                    130                    135                    140  
  
 tcc cac gac ccg gtg gtc cgc gcc cgc ggg tac cgc gtg cac aac cgg 763  
 Ser His Asp Pro Val Val Arg Ala Arg Gly Tyr Arg Val His Asn Arg  
                     145                    150                    155  
  
 gag ttc cat gcg gcc atc cac gcg atg gcg cac tcg cgg atc atg gag 811  
 Glu Phe His Ala Ala Ile His Ala Met Ala His Ser Arg Ile Met Glu  
                     160                    165                    170  
  
 gag acc agc cag cga atg tgg gat ctg tcg gac ttc ttg atc aac acc 859  
 Glu Thr Ser Gln Arg Met Trp Asp Leu Ser Asp Phe Leu Ile Asn Thr  
                     175                    180                    185  
  
 acc ggc atc acc aac ccg ctc tcg agc gca ctg ccc gac cgg cag cat 907  
 Thr Gly Ile Thr Asn Pro Leu Ser Ser Ala Leu Pro Asp Arg Gln His  
                     190                    195                    200

gac cac cac gaa atc acc gag gcc atc cgc aac cgt gac gca gct gcc 955  
 Asp His His Glu Ile Thr Glu Ala Ile Arg Asn Arg Asp Ala Ala Ala  
 205 210 215 220

gcc cgc gag gcc atg gaa cgc cac atc gtc ggc acc atc gca gta atc 1003  
 Ala Arg Glu Ala Met Glu Arg His Ile Val Gly Thr Ile Ala Val Ile  
 225 230 235

cgc gac gaa tcc aac gcc cag ctg ccg agc tag accccgatac ccggggccatc 1056  
 Arg Asp Glu Ser Asn Ala Gln Leu Pro Ser  
 240 245

gaccggctcc gctatcgcc cacctacgcc gaggggggac tctcgccgt agcgctgcag 1116

acgatccacc ggcaccctcc acgtgaccc ctgtctcgcc ctagagggcc ggcgcgccgt 1176

cgatcacctt taccctcatc cagagacttg cgtcacctc tatgcccagag tagcgtctga 1236

actagacgtc tagcattcta gttga gtg ctc cct ctc gaa gat tct cca gag 1288  
 Val Leu Pro Leu Glu Asp Ser Pro Glu  
 250 255

aac ccc tct cga aca tcc cca gaa gaa agg agc ggc cat gac gac cgc 1336  
 Asn Pro Ser Arg Thr Ser Pro Glu Glu Arg Ser Gly His Asp Asp Arg  
 260 265 270

ttc gca cgc atc gtc ctt cgg ggc acg agc cca ctt ccg ccc aca gat 1384  
 Phe Ala Arg Ile Val Leu Arg Gly Thr Ser Pro Leu Pro Pro Thr Asp  
 275 280 285

cgg gga agc ccg acc gtg agc acc aca cct acc tcc ccg acg aag acc 1432  
 Arg Gly Ser Pro Thr Val Ser Thr Thr Pro Thr Ser Pro Thr Lys Thr  
 290 295 300

tca ccg ctg cgg gta gcg atg gcc agc ttc atc ggt acc acc gtc gag 1480  
 Ser Pro Leu Arg Val Ala Met Ala Ser Phe Ile Gly Thr Thr Val Glu  
 305 310 315 320

tac tac gac ttc ttc atc tac ggc acc gcg gcc gcg ctg gta ttc cct 1528  
 Tyr Tyr Asp Phe Phe Ile Tyr Gly Thr Ala Ala Ala Leu Val Phe Pro  
 325 330 335

gag ttg ttc ttc ccg gat gtc tcg tcc gcg atc gga atc ctg ttg tcg 1576  
 Glu Leu Phe Phe Pro Asp Val Ser Ser Ala Ile Gly Ile Leu Leu Ser  
 340 345 350

ttc gcg acc ttc agc gtt ggg ttc ctc gcc cgc ccg ctg ggt ggc ata 1624  
 Phe Ala Thr Phe Ser Val Gly Phe Leu Ala Arg Pro Leu Gly Gly Ile  
 355 360 365

gtg ttc ggg cac ttc ggt gac cgg gtc ggc cgc aag cag atg ctg gtg 1672  
 Val Phe Gly His Phe Gly Asp Arg Val Gly Arg Lys Gln Met Leu Val  
 370 375 380

atc tcc ctg gtc gga atg ggc tcg gcc acc gta ctg atg gga ttg ttg 1720  
 Ile Ser Leu Val Gly Met Gly Ser Ala Thr Val Leu Met Gly Leu Leu  
 385 390 395 400

|  |      |
|--|------|
| ccc ggt tac gcc caa atc ggg atc gcc gcc ccc atc ctg ctg acc ctg<br>Pro Gly Tyr Ala Gln Ile Gly Ile Ala Ala Pro Ile Leu Leu Thr Leu | 1768 |
| 405 410 415  |      |
| ctg cgc ctg gtg cag ggc ttt gcc gtc ggc ggc gag tgg ggt gga gcc<br>Leu Arg Leu Val Gln Gly Phe Ala Val Gly Gly Glu Trp Gly Gly Ala | 1816 |
| 420 425 430  |      |
| acc ctg atg gcc gtc gag cac gcc ccc acc gcg aag aag ggc ttt ttc<br>Thr Leu Met Ala Val Glu His Ala Pro Thr Ala Lys Lys Gly Phe Phe | 1864 |
| 435 440 445  |      |
| gga tcc ttc tcc cag atg ggg gca ccc gcc ggg acc agc gtc gca acc<br>Gly Ser Phe Ser Gln Met Gly Ala Pro Ala Gly Thr Ser Val Ala Thr | 1912 |
| 450 455 460  |      |
| ctg gcg ttc ttc gcg gtc tcc caa ttg ccc gac gag cag ttc ctg agt<br>Leu Ala Phe Phe Ala Val Ser Gln Leu Pro Asp Glu Gln Phe Leu Ser | 1960 |
| 465 470 475 480  |      |
| tgg ggc tgg cga ctg ccg ttc ctg ttc agc gcg gtg ctg atc gtg atc<br>Trp Gly Trp Arg Leu Pro Phe Leu Phe Ser Ala Val Leu Ile Val Ile | 2008 |
| 485 490 495  |      |
| ggg ctg ttc att cgc ctg tcc ctg gcc gaa agc ccc gac ttc gcc gag<br>Gly Leu Phe Ile Arg Leu Ser Leu Ala Glu Ser Pro Asp Phe Ala Glu | 2056 |
| 500 505 510  |      |
| gtg aag gca cag agc gcc gtg gtg cga atg ccg atc gcc gaa gcg ttc<br>Val Lys Ala Gln Ser Ala Val Val Arg Met Pro Ile Ala Glu Ala Phe | 2104 |
| 515 520 525  |      |
| cgc aag cac tgg aag gaa att ctc ctc atc gcg ggc acc tac ctg tcc<br>Arg Lys His Trp Lys Glu Ile Leu Leu Ile Ala Gly Thr Tyr Leu Ser | 2152 |
| 530 535 540  |      |
| caa gga gtg ttc gcc tat atc tgc atg gcc tac ctc gtc tcc tac ggc<br>Gln Gly Val Phe Ala Tyr Ile Cys Met Ala Tyr Leu Val Ser Tyr Gly | 2200 |
| 545 550 555 560  |      |
| acc acc gtc gcg ggg atc agc cgc acc ttc gcc ctg gcc gga gta ttc<br>Thr Thr Val Ala Gly Ile Ser Arg Thr Phe Ala Leu Ala Gly Val Phe | 2248 |
| 565 570 575  |      |
| gtc gcc ggc atc gtc gcc gtc ctc ctc tac ctc gtg ttc ggc gct ctg<br>Val Ala Gly Ile Val Ala Val Leu Leu Tyr Leu Val Phe Gly Ala Leu | 2296 |
| 580 585 590  |      |
| tcc gac act ttc ggc cgc aag acc atg tac ctg ctc ggc gcc gcc gcg<br>Ser Asp Thr Phe Gly Arg Lys Thr Met Tyr Leu Leu Gly Ala Ala Ala | 2344 |
| 595 600 605  |      |
| atg ggt gtg gtg atc gcc ccc gcc ttc gca ctg atc aac acc ggc aac<br>Met Gly Val Val Ile Ala Pro Ala Phe Ala Leu Ile Asn Thr Gly Asn | 2392 |
| 610 615 620  |      |

|   |      |
|---|------|
| ccg tgg ctg ttc atg gcc gcg cag gtg ctg gtc ttc gga att gca atg<br>Pro Trp Leu Phe Met Ala Ala Gln Val Leu Val Phe Gly Ile Ala Met<br>625 630 635 640 | 2440 |
| gcc ccc gcc gcc ggc gtg aca ggc tcc ctg ttc acg atg gtc ttc gac<br>Ala Pro Ala Ala Gly Val Thr Gly Ser Leu Phe Thr Met Val Phe Asp<br>645 650 655     | 2488 |
| gcg gac gtg cgc tac agc ggt gtc tct atc ggc tac acc atc tcc cag<br>Ala Asp Val Arg Tyr Ser Gly Val Ser Ile Gly Tyr Thr Ile Ser Gln<br>660 665 670     | 2536 |
| gtc gcc ggc tcc gcg ttc gcc ccg acg atc gcg acc gcc ttg tac gcc<br>Val Ala Gly Ser Ala Phe Ala Pro Thr Ile Ala Thr Ala Leu Tyr Ala<br>675 680 685     | 2584 |
| tcc acc aac acc agc aac tcg atc gtg acc tac ctg ctg atc gtc tcg<br>Ser Thr Asn Thr Ser Asn Ser Ile Val Thr Tyr Leu Leu Ile Val Ser<br>690 695 700     | 2632 |
| gcc atc tcg atc gtc tcg gtg atc ctg ctg ccc ggc ggc tgg ggg cgc<br>Ala Ile Ser Ile Val Ser Val Ile Leu Leu Pro Gly Gly Trp Gly Arg<br>705 710 715 720 | 2680 |
| aag ggc gct gcg agc cag ctc act cgc gac cag gcc acc tcc aca ccg<br>Lys Gly Ala Ala Ser Gln Leu Thr Arg Asp Gln Ala Thr Ser Thr Pro<br>725 730 735     | 2728 |
| aaa atg cct gac acc gaa aca ttt tcg act cgg aca gtt ccg gac acc<br>Lys Met Pro Asp Thr Glu Thr Phe Ser Thr Arg Thr Val Pro Asp Thr<br>740 745 750     | 2776 |
| gca gca tcc ctg cgc gtc ctc gac aag tga a gtg atg aca gac atg agt<br>Ala Ala Ser Leu Arg Val Leu Asp Lys Val Met Thr Asp Met Ser<br>755 760 765       | 2825 |
| gac cac gac cgc acc tcc tac gac acc gac gtc gtg atc gtc ggc ctc<br>Asp His Asp Arg Thr Ser Tyr Asp Thr Asp Val Val Ile Val Gly Leu<br>770 775 780     | 2873 |
| ggc ccc gcc ggt ggc aca gcg gcg ctt gcc ctg gcc agc tac ggc atc<br>Gly Pro Ala Gly Gly Thr Ala Ala Leu Ala Ser Tyr Gly Ile<br>785 790 795 800         | 2921 |
| cgc gtt cac gcc gtc tcg atg ttc ccc tgg gtg gcg aac tcg ccg cgc<br>Arg Val His Ala Val Ser Met Phe Pro Trp Val Ala Asn Ser Pro Arg<br>805 810 815     | 2969 |
| gcg cac atc acc aac cag cgc gcc gtc gaa gtg ctg cgt gac ctg ggc<br>Ala His Ile Thr Asn Gln Arg Ala Val Glu Val Leu Arg Asp Leu Gly<br>820 825 830     | 3017 |
| gtc gaa gac gag gcg cgc aac tac gcc acc ccg tgg gac cag atg ggc<br>Val Glu Asp Glu Ala Arg Asn Tyr Ala Thr Pro Trp Asp Gln Met Gly<br>835 840 845     | 3065 |

|   |      |
|---|------|
| gac acg ctg ttc acc acg agc ctg gcc ggc gag gag atc gtc cgg atg<br>Asp Thr Leu Phe Thr Thr Ser Leu Ala Gly Glu Glu Ile Val Arg Met<br>850 855 860         | 3113 |
| cag acc tgg ggt acg ggc gat atc cgc tac ggg gac tac ctg tcc gga<br>Gln Thr Trp Gly Thr Gly Asp Ile Arg Tyr Gly Asp Tyr Leu Ser Gly<br>865 870 875 880     | 3161 |
| agc ccc tgc acg atg ctc gac att ccg cag ccc ctg atg gag ccg gtg<br>Ser Pro Cys Thr Met Leu Asp Ile Pro Gln Pro Leu Met Glu Pro Val<br>885 890 895         | 3209 |
| ctg atc aag aac gcc gcc gaa cgt ggt gcg gtc atc agc ttc aac acc<br>Leu Ile Lys Asn Ala Ala Glu Arg Gly Ala Val Ile Ser Phe Asn Thr<br>900 905 910         | 3257 |
| gaa tac ctc gac cac gcc cag gac gag gac ggg gtg acc gtc cgg ttc<br>Glu Tyr Leu Asp His Ala Gln Asp Glu Asp Gly Val Thr Val Arg Phe<br>915 920 925         | 3305 |
| cgc gac gtc cgc tcg ggc acc gtg ttc acc cag cga gcc cgc ttc ctg<br>Arg Asp Val Arg Ser Gly Thr Val Phe Thr Gln Arg Ala Arg Phe Leu<br>930 935 940         | 3353 |
| ctc ggt ttc gac ggc gca cga tcg aag atc gcc gaa cag atc ggg ctt<br>Leu Gly Phe Asp Gly Ala Arg Ser Lys Ile Ala Glu Gln Ile Gly Leu<br>945 950 955 960     | 3401 |
| ccg ttc gaa ggt gaa ctc gcc cgc gcc ggt acc gcg tac atc ctg ttc<br>Pro Phe Glu Gly Glu Leu Ala Arg Ala Gly Thr Ala Tyr Ile Leu Phe<br>965 970 975         | 3449 |
| aac gcg gac ctg agc aaa tat gtc gct cat cgg ccg agc atc ttg cac<br>Asn Ala Asp Leu Ser Lys Tyr Val Ala His Arg Pro Ser Ile Leu His<br>980 985 990         | 3497 |
| tgg atc gtc aac tcg aag gcc ggt ttc ggt gag atc ggc atg ggt ctg<br>Trp Ile Val Asn Ser Lys Ala Gly Phe Gly Glu Ile Gly Met Gly Leu<br>995 1000 1005       | 3545 |
| ctg cgc gcg atc cga ccg tgg gac cag tgg atc gcc ggc tgg ggc ttc<br>Leu Arg Ala Ile Arg Pro Trp Asp Gln Trp Ile Ala Gly Trp Gly Phe<br>1010 1015 1020      | 3593 |
| gac atg gcg aac ggc gag ccg gat gtc tcc gac gac gtt gtc ctc gaa<br>Asp Met Ala Asn Gly Glu Pro Asp Val Ser Asp Asp Val Val Leu Glu<br>1025 1030 1035 1040 | 3641 |
| cag atc cgg acc ctc gtc ggc gac ccg cac ctg gac gtc gag atc gtg<br>Gln Ile Arg Thr Leu Val Gly Asp Pro His Leu Asp Val Glu Ile Val<br>1045 1050 1055      | 3689 |
| tcg agg tcc ttc tgg tac gtc aac ccg cag tgg gct gag cac tac cag<br>Ser Arg Ser Phe Trp Tyr Val Asn Arg Gln Trp Ala Glu His Tyr Gln<br>1060 1065 1070      | 3737 |

|   |      |
|---|------|
| tcc ggt cga gtg ttc tgc ggc ggc gac gcg gtg cac cgg cat ccg ccg | 3785 |
| Ser Gly Arg Val Phe Cys Gly Gly Asp Ala Val His Arg His Pro Pro |      |
| 1075 1080 1085  |      |
| agc agc ggg ctg ggc tcg aac acg tcc atg cag gac gcg ttc aac ctg | 3833 |
| Ser Ser Gly Leu Gly Ser Asn Thr Ser Met Gln Asp Ala Phe Asn Leu |      |
| 1090 1095 1100  |      |
| gca tgg aag atc gcg ttc gtc gtg aag ggg tat gca gga ccg ggt ctg | 3881 |
| Ala Trp Lys Ile-Ala Phe Val Val Lys Gly Tyr Ala Gly Pro Gly Leu |      |
| 1105 1110 1115 1120   |      |
| ctc gag tcc tac tct cct gag cgt gtt ccg gtc ggc aaa cag atc gtc | 3929 |
| Leu Glu Ser Tyr Ser Pro Glu Arg Val Pro Val Gly Lys Gln Ile Val |      |
| 1125 1130 1135  |      |
| gct cgc gcc aac cag tcc cgc aag gac tac gcc ggg ctg cgc gaa tgg | 3977 |
| Ala Arg Ala Asn Gln Ser Arg Lys Asp Tyr Ala Gly Leu Arg Glu Trp |      |
| 1140 1145 1150  |      |
| ttc gat cac gag agc gac gac ccg gtc gcc gcc ggc ctg gca aag ttg | 4025 |
| Phe Asp His Glu Ser Asp Asp Pro Val Ala Ala Gly Leu Ala Lys Leu |      |
| 1155 1160 1165  |      |
| aag gaa ccc tcg tcc gaa ggt gtt gct ctg cgt gag cgg ctg tac gag | 4073 |
| Lys Glu Pro Ser Ser Glu Gly Val Ala Leu Arg Glu Arg Leu Tyr Glu |      |
| 1170 1175 1180  |      |
| gcg ctg gag gtg aag aac gcc gaa ttc aac gcc cag ggc gtc gaa ctc | 4121 |
| Ala Leu Glu Val Lys Asn Ala Glu Phe Asn Ala Gln Gly Val Glu Leu |      |
| 1185 1190 1195 1200   |      |
| aac cag cgc tac acc tcg tcc gcg gtc gtt ccc gac ccc gag gcg ggc | 4169 |
| Asn Gln Arg Tyr Thr Ser Ser Ala Val Val Pro Asp Pro Glu Ala Gly |      |
| 1205 1210 1215  |      |
| gag gaa gtg tgg gtg cgc gat cgt gag ctg tac ctg cag gcc acc acc | 4217 |
| Glu Glu Val Trp Val Arg Asp Arg Glu Leu Tyr Leu Gln Ala Thr Thr |      |
| 1220 1225 1230  |      |
| cgg ccg ggc gcg aag ctg ccg cat gcg tgg ctg gtc ggc gcc gac gga | 4265 |
| Arg Pro Gly Ala Lys Leu Pro His Ala Trp Leu Val Gly Ala Asp Gly |      |
| 1235 1240 1245  |      |
| acc cgc atc tcc acc ctc gac gtc acc ggc aag gga atg atg acc ctg | 4313 |
| Thr Arg Ile Ser Thr Leu Asp Val Thr Gly Lys Gly Met Met Thr Leu |      |
| 1250 1255 1260  |      |
| ctg acc gga ctc ggc ggc cag gca tgg aag cgt gcc gcc gcc aaa ctc | 4361 |
| Leu Thr Gly Leu Gly Gln Ala Trp Lys Arg Ala Ala Ala Lys Leu     |      |
| 1265 1270 1275 1280   |      |
| gac ctg ccg ttc ctg cgg acc gtc gtt gtc ggc gaa ccc ggc acc atc | 4409 |
| Asp Leu Pro Phe Leu Arg Thr Val Val Val Gly Glu Pro Gly Thr Ile |      |
| 1285 1290 1295  |      |



gac cct tac gga tac tgg cgg cgg gtc cgc gac atc gac gag gcc ggc 4457  
 Asp Pro Tyr Gly Tyr Trp Arg Arg Val Arg Asp Ile Asp Glu Ala Gly  
 1300 1305 1310  
 gcc ctg ctc gtg cgg ccc gac ggc tac gtc gcg tgg cga cac agt gct 4505  
 Ala Leu Leu Val Arg Pro Asp Gly Tyr Val Ala Trp Arg His Ser Ala  
 1315 1320 1325  
 ccg gtc tgg gac gac acc gaa gcg ctc acc agc ctc gag aac gct ctc 4553  
 Pro Val Trp Asp Asp Thr Glu Ala Leu Thr Ser Leu Glu Asn Ala Leu  
 1330 1335 1340  
 acc gcg gtc ctc gac cac tcg gcc agc gac aac ggg aac ccg agc ggc 4601  
 Thr Ala Val Leu Asp His Ser Ala Ser Asp Asn Gly Asn Pro Ser Gly  
 1345 1350 1355 1360  
 aca aac gag ccg cag tac agc acc cgg gcc gtg ccg atc gtc gtt ccg 4649  
 Thr Asn Glu Pro Gln Tyr Ser Thr Arg Ala Val Pro Ile Val Val Pro  
 1365 1370 1375  
 cac gtt acc gcc gag gat gca gca cca gct tcc gcc acc cgc acc acc 4697  
 His Val Thr Ala Glu Asp Ala Ala Pro Ala Ser Ala Thr Arg Thr Thr  
 1380 1385 1390  
 aca gtc gag gga gag aac cga tga ccggtcctta caccagcgtc tgggacgacc 4751  
 Thr Val Glu Gly Glu Asn Arg  
 1395 1400  
 tgaaccaggt cgagttcagc cagggattca tccaggccgg cccctaccgg acccgataacc 4811  
 tgcacgccgg cgattcgtcc aagcccacgc tgatcctgct gcacggcatc accggccacg 4871  
 ccgaggcgta cgtgcgcaat ctgcgctcgc attccgagca cttcaacgtc tgggcaatcg 4931  
 acttcatcgg ccacggctat tcgaccaagc ccgaccaccc gctcgagatc aagcactaca 4991  
 tcgaccacgt gctgcagttg ctggacgcca tcggcgctcga gaaggcctcg ttttcggggg 5051  
 agtctctcgg cggttgggtc accgcccagt tcgcgcacga ccatcccagag aaggctcgacc 5111  
 ggatcgtgct caacaccatg ggcggcacca tggccaaccc tcaggtgatg gaacgtctct 5171  
 ataccctgtc gatggaagcg gcgaaggacc cgagctggga acgcgtaaaa gcacgcctcg 5231  
 aatggctcat ggccgacccg accatggtca ccgacgacct gatccgcacc cgccaggcca 5291  
 tcttccagca gccggattgg ctcaaggcct gcgagatgaa catggcactg caggacctcg 5351  
 aaaccgcaa gcggaacatg atcaccgacg ccaactctcaa cggcatcacg gtgcccgcga 5411  
 tgggtgctgtg gaccaccaag gacccctccg gtccgggtcga cgaagccaag cgcacgcct 5471  
 cccacatccc gggcgccaag ctggccatca tggagaactg tggccactgg cccagtagc 5531  
 aggaccccga gacettcaac aagctgcatc tggacttctt cctcgggtcg agctgacaca 5591  
 gaccccgggc ggtgcccga acccctgcaa cccggggcgg accggccgga tctcacttac 5651

ccgacctatt gcgctctcgt ccggaccccc ggagagaaag cgccgaagca gcagcaagga 5711

gaccgcccgcg atg cct gta gcg ctg tgc gcg atg tcg cac tcc ccc ctg 5760  
Met Pro Val Ala Leu Cys Ala Met Ser His Ser Pro Leu  
1405 1410

atg gga cgc aac gac ccc gaa cag gaa gtc atc gac gcc gtc gac gcc 5808  
Met Gly Arg Asn Asp Pro Glu Gln Glu Val Ile Asp Ala Val Asp Ala  
1415 1420 1425

gca ttc gac cac gcg cgc cgg ttc gtc gcc gac ttc gcc ccc gat ctg 5856  
Ala Phe Asp His Ala Arg Arg Phe Val Ala Asp Phe Ala Pro Asp Leu  
1430 1435 1440 1445

atc gtc atc ttc gcc ccc gac cac tac aac ggc gtc ttc tac gac ctg 5904  
Ile Val Ile Phe Ala Pro Asp His Tyr Asn Gly Val Phe Tyr Asp Leu  
1450 1455 1460

ctg ccg ccg ttc tgt atc ggt gcc gcc gcg cag tcc gtc ggc gac tac 5952  
Leu Pro Pro Phe Cys Ile Gly Ala Ala Ala Gln Ser Val Gly Asp Tyr  
1465 1470 1475

ggc acc gaa gcc ggc cct ctg gac gtc gac cgt gac gcc gcc tac gca 6000  
Gly Thr Glu Ala Gly Pro Leu Asp Val Asp Arg Asp Ala Ala Tyr Ala  
1480 1485 1490

gtc gcc cgc gac gtc ctg gac agc ggc atc gac gtc gca ttc tcc gaa 6048  
Val Ala Arg Asp Val Leu Asp Ser Gly Ile Asp Val Ala Phe Ser Glu  
1495 1500 1505

cgc atg cac gtc gac cac gga ttc gcc caa gca ctg caa ttg ctg gtc 6096  
Arg Met His Val Asp His Gly Phe Ala Gln Ala Leu Gln Leu Leu Val  
1510 1515 1520 1525

gga tcg atc acc gcc gtg ccg acc gtg ccg atc ttc atc aat tcg gtc 6144  
Gly Ser Ile Thr Ala Val Pro Thr Val Pro Ile Phe Ile Asn Ser Val  
1530 1535 1540

gcc gaa ccg ctg ggc ccg gtc agc cgg gta cgg ctg ctg ggc gag gcg 6192  
Ala Glu Pro Leu Gly Pro Val Ser Arg Val Arg Leu Leu Gly Glu Ala  
1545 1550 1555

gtc ggg cgg gcc gct gcc aag ctg gac aag cgt gtg ctg ttc gtc gga 6240  
Val Gly Arg Ala Ala Ala Lys Leu Asp Lys Arg Val Leu Phe Val Gly  
1560 1565 1570

tcc ggc ggc ctg tcc cac gac ccg ccg gtc ccg cag ttc gcc acc gcg 6288  
Ser Gly Gly Leu Ser His Asp Pro Pro Val Pro Gln Phe Ala Thr Ala  
1575 1580 1585

cca gag gaa gtg cgc gag cgg ttg atc gac ggc cgc aat ccc agt gcc 6336  
Pro Glu Glu Val Arg Glu Arg Leu Ile Asp Gly Arg Asn Pro Ser Ala  
1590 1595 1600 1605

gcc gaa cgt gat gcc cgc gaa cag cgc gtc atc acc gcc ggg cgg gac 6384  
 Ala Glu Arg Asp Ala Arg Glu Gln Arg Val Ile Thr Ala Gly Arg Asp  
 1610 1615 1620

ttc gcc gcc ggc acc gcc gcc atc cag cca ctg aac ccc gaa tgg gac 6432  
 Phe Ala Ala Gly Thr Ala Ala Ile Gln Pro Leu Asn Pro Glu Trp Asp  
 1625 1630 1635

cgg cac ctg ctc gac gtc ctc gcc tcc ggc gac ctc gag cag atc gac 6480  
 Arg His Leu Leu Asp Val Leu Ala Ser Gly Asp Leu Glu Gln Ile Asp  
 1640 1645 1650

gcg tgg acc aac gac tgg ttc gtc gaa cag gcc gga cac tcc tcc cac 6528  
 Ala Trp Thr Asn Asp Trp Phe Val Glu Gln Ala Gly His Ser Ser His  
 1655 1660 1665

gaa gtg cgc acc tgg atc gcc gcg tac gcg gca atg agc gcc gcc ggg 6576  
 Glu Val Arg Thr Trp Ile Ala Ala Tyr Ala Ala Met Ser Ala Ala Gly  
 1670 1675 1680 1685

aag tac cgc gtc acc tcg acc ttc tac cgc gaa atc cac gag tgg ata 6624  
 Lys Tyr Arg Val Thr Ser Thr Phe Tyr Arg Glu Ile His Glu Trp Ile  
 1690 1695 1700

gca gga ttc ggg att act acc gcc gtc gcc gtc gac gaa tag 6666  
 Ala Gly Phe Gly Ile Thr Thr Ala Val Ala Val Asp Glu  
 1705 1710 1715

accccgccgc tcccgccccg cagtcccaac gaagggtggc cccggatgac ctccgtccgc 6726  
 ccgtgctcgc cgtcgggtgaa cgcgggctgg tcggtgggca ggaagacctc atcgccgaca 6786  
 tcgccctcga cctcgcagct cgtcagtagg aatgcgcacg ggccgacgag tcgcgctggt 6846  
 caccggggcc agccgcggca tcggggcggc catcgcagat gcggtggccg cctccggtgc 6906  
 cgccgtaatc gtccactacg gatccgatcg gacggccgcc gctgcggtgt cgacggcatc 6966  
 acggctgccg ggggcctcgc ggctgcggtc caggccgacc tgtcccgacc cgaggggcct 7026  
 gaagagctga tgcgggagtt cgactccgcg ctcgacggtc tcgggctcga ccgagggctc 7086  
 gacatcctcg tcaacaacgc cggaatcagt cggcgcgag cgctcgagcg cgtcactgtc 7146  
 gaggatttcg accgtctggt cgcactcaac cagcgcgcc cgctcttcgt gactcggcat 7206  
 gccctgcccc ggatgcacga cggcggtcgc atcgtcaaca ttctctcgg atccgccccg 7266  
 tacgccagac ccgacgtcat cagctacgcc atgaccaagg gggcgatcga ggtgtcacc 7326  
 cgcgccctcg ccgtagacgt cggcgaacga ggcacaccg ccaacgccgt ggcgccggcc 7386  
 gcgctcgata ccgacatgaa cgcgcactgg cttcgcggtg acgaccatgc ccgcaccacc 7446  
 gccgcgtcca ccaactgcact gcgaaaactc gccaccgcgg aggacatcgc cgcgatcgtg 7506  
 gccttctcgc tcagcgccgc cgccggtgcg atcaccgggc aggtcatcga cgccaccaac 7566

ggcaaccggc tctaaccaga acttaccggg tccc

7600

<210> 2

<211> 247

<212> PRT

<213> Rhodococcus sp.

<400> 2

Met Thr Thr Thr Asp Thr Gly Pro Lys Pro Gly Ser Glu Ala Ala  
1 5 10 15  
Ala Leu Leu Ala Asn Val Arg Thr Ser Gly Ala Arg Leu Ser Ser Ala  
20 25 30  
Leu Tyr Asp Ile Leu Lys Asn Arg Leu Leu Glu Gly Arg Tyr Ala Ala  
35 40 45  
Gly Glu Lys Ile Val Val Glu Ser Ile Arg Gln Glu Phe Gly Val Ser  
50 55 60  
Lys Gln Pro Val Met Asp Ala Leu Arg Arg Leu Ser Ser Asp Lys Leu  
65 70 75  
Val His Ile Val Pro Gln Val Gly Cys Glu Val Val Ser Tyr Ala Pro  
80 85 90 95  
Arg Glu Val Glu Asp Phe Tyr Thr Leu Phe Gly Gly Phe Glu Gly Thr  
100 105 110  
Ile Ala Ala Val Ala Ala Ser Arg Arg Thr Glu Ala Gln Leu Leu Glu  
115 120 125  
Leu Asp Leu Ile Ser Ala Arg Val Asp Ala Leu Ile Thr Ser His Asp  
130 135 140  
Pro Val Val Arg Ala Arg Gly Tyr Arg Val His Asn Arg Glu Phe His  
145 150 155  
Ala Ala Ile His Ala Met Ala His Ser Arg Ile Met Glu Glu Thr Ser  
160 165 170 175  
Gln Arg Met Trp Asp Leu Ser Asp Phe Leu Ile Asn Thr Thr Gly Ile  
180 185 190  
Thr Asn Pro Leu Ser Ser Ala Leu Pro Asp Arg Gln His Asp His His  
195 200 205  
Glu Ile Thr Glu Ala Ile Arg Asn Arg Asp Ala Ala Ala Arg Glu  
210 215 220  
Ala Met Glu Arg His Ile Val Gly Thr Ile Ala Val Ile Arg Asp Glu  
225 230 235  
Ser Asn Ala Gln Leu Pro Ser  
240 245

<210> 3

<211> 515

<212> PRT

<213> Rhodococcus sp.

<400> 3

Val Leu Pro Leu Glu Asp Ser Pro Glu Asn Pro Ser Arg Thr Ser  
1 5 10 15  
Pro Glu Glu Arg Ser Gly His Asp Asp Arg Phe Ala Arg Ile Val Leu  
20 25 30  
Arg Gly Thr Ser Pro Leu Pro Pro Thr Asp Arg Gly Ser Pro Thr Val  
35 40 45  
Ser Thr Thr Pro Thr Ser Pro Thr Lys Thr Ser Pro Leu Arg Val Ala  
50 55 60

Met Ala Ser Phe Ile Gly Thr Thr Val Glu Tyr Tyr Asp Phe Phe Ile  
 65 70 75  
 Tyr Gly Thr Ala Ala Ala Leu Val Phe Pro Glu Leu Phe Phe Pro Asp  
 80 85 90 95  
 Val Ser Ser Ala Ile Gly Ile Leu Leu Ser Phe Ala Thr Phe Ser Val  
 100 105 110  
 Gly Phe Leu Ala Arg Pro Leu Gly Gly Ile Val Phe Gly His Phe Gly  
 115 120 125  
 Asp Arg Val Gly Arg Lys Gln Met Leu Val Ile Ser Leu Val Gly Met  
 130 135 140  
 Gly Ser Ala Thr Val Leu Met Gly Leu Leu Pro Gly Tyr Ala Gln Ile  
 145 150 155  
 Gly Ile Ala Ala Pro Ile Leu Leu Thr Leu Leu Arg Leu Val Gln Gly  
 160 165 170 175  
 Phe Ala Val Gly Gly Glu Trp Gly Gly Ala Thr Leu Met Ala Val Glu  
 180 185 190  
 His Ala Pro Thr Ala Lys Lys Gly Phe Phe Gly Ser Phe Ser Gln Met  
 195 200 205  
 Gly Ala Pro Ala Gly Thr Ser Val Ala Thr Leu Ala Phe Phe Ala Val  
 210 215 220  
 Ser Gln Leu Pro Asp Glu Gln Phe Leu Ser Trp Gly Trp Arg Leu Pro  
 225 230 235  
 Phe Leu Phe Ser Ala Val Leu Ile Val Ile Gly Leu Phe Ile Arg Leu  
 240 245 250 255  
 Ser Leu Ala Glu Ser Pro Asp Phe Ala Glu Val Lys Ala Gln Ser Ala  
 260 265 270  
 Val Val Arg Met Pro Ile Ala Glu Ala Phe Arg Lys His Trp Lys Glu  
 275 280 285  
 Ile Leu Leu Ile Ala Gly Thr Tyr Leu Ser Gln Gly Val Phe Ala Tyr  
 290 295 300  
 Ile Cys Met Ala Tyr Leu Val Ser Tyr Gly Thr Thr Val Ala Gly Ile  
 305 310 315  
 Ser Arg Thr Phe Ala Leu Ala Gly Val Phe Val Ala Gly Ile Val Ala  
 320 325 330 335  
 Val Leu Leu Tyr Leu Val Phe Gly Ala Leu Ser Asp Thr Phe Gly Arg  
 340 345 350  
 Lys Thr Met Tyr Leu Leu Gly Ala Ala Ala Met Gly Val Val Ile Ala  
 355 360 365  
 Pro Ala Phe Ala Leu Ile Asn Thr Gly Asn Pro Trp Leu Phe Met Ala  
 370 375 380  
 Ala Gln Val Leu Val Phe Gly Ile Ala Met Ala Pro Ala Ala Gly Val  
 385 390 395  
 Thr Gly Ser Leu Phe Thr Met Val Phe Asp Ala Asp Val Arg Tyr Ser  
 400 405 410 415  
 Gly Val Ser Ile Gly Tyr Thr Ile Ser Gln Val Ala Gly Ser Ala Phe  
 420 425 430  
 Ala Pro Thr Ile Ala Thr Ala Leu Tyr Ala Ser Thr Asn Thr Ser Asn  
 435 440 445  
 Ser Ile Val Thr Tyr Leu Leu Ile Val Ser Ala Ile Ser Ile Val Ser  
 450 455 460  
 Val Ile Leu Leu Pro Gly Gly Trp Gly Arg Lys Gly Ala Ala Ser Gln  
 465 470 475  
 Leu Thr Arg Asp Gln Ala Thr Ser Thr Pro Lys Met Pro Asp Thr Glu  
 480 485 490 495  
 Thr Phe Ser Thr Arg Thr Val Pro Asp Thr Ala Ala Ser Leu Arg Val  
 500 505 510

Leu Asp Lys  
515

<210> 4  
<211> 638  
<212> PRT  
<213> Rhodococcus sp.

<400> 4

Val Met Thr Asp Met Ser Asp His Asp Arg Thr Ser Tyr Asp Thr  
1 5 10 15  
Asp Val Val Ile Val Gly Leu Gly Pro Ala Gly Gly Thr Ala Ala Leu  
20 25 30  
Ala Leu Ala Ser Tyr Gly Ile Arg Val His Ala Val Ser Met Phe Pro  
35 40 45  
Trp Val Ala Asn Ser Pro Arg Ala His Ile Thr Asn Gln Arg Ala Val  
50 55 60  
Glu Val Leu Arg Asp Leu Gly Val Glu Asp Glu Ala Arg Asn Tyr Ala  
65 70 75  
Thr Pro Trp Asp Gln Met Gly Asp Thr Leu Phe Thr Thr Ser Leu Ala  
80 85 90 95  
Gly Glu Glu Ile Val Arg Met Gln Thr Trp Gly Thr Gly Asp Ile Arg  
100 105 110  
Tyr Gly Asp Tyr Leu Ser Gly Ser Pro Cys Thr Met Leu Asp Ile Pro  
115 120 125  
Gln Pro Leu Met Glu Pro Val Leu Ile Lys Asn Ala Ala Glu Arg Gly  
130 135 140  
Ala Val Ile Ser Phe Asn Thr Glu Tyr Leu Asp His Ala Gln Asp Glu  
145 150 155  
Asp Gly Val Thr Val Arg Phe Arg Asp Val Arg Ser Gly Thr Val Phe  
160 165 170 175  
Thr Gln Arg Ala Arg Phe Leu Leu Gly Phe Asp Gly Ala Arg Ser Lys  
180 185 190  
Ile Ala Glu Gln Ile Gly Leu Pro Phe Glu Gly Glu Leu Ala Arg Ala  
195 200 205  
Gly Thr Ala Tyr Ile Leu Phe Asn Ala Asp Leu Ser Lys Tyr Val Ala  
210 215 220  
His Arg Pro Ser Ile Leu His Trp Ile Val Asn Ser Lys Ala Gly Phe  
225 230 235  
Gly Glu Ile Gly Met Gly Leu Leu Arg Ala Ile Arg Pro Trp Asp Gln  
240 245 250 255  
Trp Ile Ala Gly Trp Gly Phe Asp Met Ala Asn Gly Glu Pro Asp Val  
260 265 270  
Ser Asp Asp Val Val Leu Glu Gln Ile Arg Thr Leu Val Gly Asp Pro  
275 280 285  
His Leu Asp Val Glu Ile Val Ser Arg Ser Phe Trp Tyr Val Asn Arg  
290 295 300  
Gln Trp Ala Glu His Tyr Gln Ser Gly Arg Val Phe Cys Gly Gly Asp  
305 310 315  
Ala Val His Arg His Pro Pro Ser Ser Gly Leu Gly Ser Asn Thr Ser  
320 325 330 335  
Met Gln Asp Ala Phe Asn Leu Ala Trp Lys Ile Ala Phe Val Val Lys  
340 345 350  
Gly Tyr Ala Gly Pro Gly Leu Leu Glu Ser Tyr Ser Pro Glu Arg Val  
355 360 365

Pro Val Gly Lys Gln Ile Val Ala Arg Ala Asn Gln Ser Arg Lys Asp  
 370 375 380  
 Tyr Ala Gly Leu Arg Glu Trp Phe Asp His Glu Ser Asp Asp Pro Val  
 385 390 395  
 Ala Ala Gly Leu Ala Lys Leu Lys Glu Pro Ser Ser Glu Gly Val Ala  
 400 405 410 415  
 Leu Arg Glu Arg Leu Tyr Glu Ala Leu Glu Val Lys Asn Ala Glu Phe  
 420 425 430  
 Asn Ala Gln Gly Val Glu Leu Asn Gln Arg Tyr Thr Ser Ser Ala Val  
 435 440 445  
 Val Pro Asp Pro Glu Ala Gly Glu Glu Val Trp Val Arg Asp Arg Glu  
 450 455 460  
 Leu Tyr Leu Gln Ala Thr Thr Arg Pro Gly Ala Lys Leu Pro His Ala  
 465 470 475  
 Trp Leu Val Gly Ala Asp Gly Thr Arg Ile Ser Thr Leu Asp Val Thr  
 480 485 490 495  
 Gly Lys Gly Met Met Thr Leu Leu Thr Gly Leu Gly Gly Gln Ala Trp  
 500 505 510  
 Lys Arg Ala Ala Lys Leu Asp Leu Pro Phe Leu Arg Thr Val Val  
 515 520 525  
 Val Gly Glu Pro Gly Thr Ile Asp Pro Tyr Gly Tyr Trp Arg Arg Val  
 530 535 540  
 Arg Asp Ile Asp Glu Ala Gly Ala Leu Leu Val Arg Pro Asp Gly Tyr  
 545 550 555  
 Val Ala Trp Arg His Ser Ala Pro Val Trp Asp Asp Thr Glu Ala Leu  
 560 565 570 575  
 Thr Ser Leu Glu Asn Ala Leu Thr Ala Val Leu Asp His Ser Ala Ser  
 580 585 590  
 Asp Asn Gly Asn Pro Ser Gly Thr Asn Glu Pro Gln Tyr Ser Thr Arg  
 595 600 605  
 Ala Val Pro Ile Val Val Pro His Val Thr Ala Glu Asp Ala Ala Pro  
 610 615 620  
 Ala Ser Ala Thr Arg Thr Thr Val Glu Gly Glu Asn Arg  
 625 630 635

<210> 5  
 <211> 315  
 <212> PRT  
 <213> Rhodococcus sp.

<400> 5  
 Met Pro Val Ala Leu Cys Ala Met Ser His Ser Pro Leu Met Gly  
 1 5 10 15  
 Arg Asn Asp Pro Glu Gln Glu Val Ile Asp Ala Val Asp Ala Ala Phe  
 20 25 30  
 Asp His Ala Arg Arg Phe Val Ala Asp Phe Ala Pro Asp Leu Ile Val  
 35 40 45  
 Ile Phe Ala Pro Asp His Tyr Asn Gly Val Phe Tyr Asp Leu Leu Pro  
 50 55 60  
 Pro Phe Cys Ile Gly Ala Ala Gln Ser Val Gly Asp Tyr Gly Thr  
 65 70 75  
 Glu Ala Gly Pro Leu Asp Val Asp Arg Asp Ala Ala Tyr Ala Val Ala  
 80 85 90 95  
 Arg Asp Val Leu Asp Ser Gly Ile Asp Val Ala Phe Ser Glu Arg Met  
 100 105 110  
 His Val Asp His Gly Phe Ala Gln Ala Leu Gln Leu Leu Val Gly Ser  
 115 120 125

Ile Thr Ala Val Pro Thr Val Pro Ile Phe Ile Asn Ser Val Ala Glu  
 130 135 140  
 Pro Leu Gly Pro Val Ser Arg Val Arg Leu Leu Gly Glu Ala Val Gly  
 145 150 155  
 Arg Ala Ala Ala Lys Leu Asp Lys Arg Val Leu Phe Val Gly Ser Gly  
 160 165 170 175  
 Gly Leu Ser His Asp Pro Pro Val Pro Gln Phe Ala Thr Ala Pro Glu  
 180 185 190  
 Glu Val Arg Glu Arg Leu Ile Asp Gly Arg Asn Pro Ser Ala Ala Glu  
 195 200 205  
 Arg Asp Ala Arg Glu Gln Arg Val Ile Thr Ala Gly Arg Asp Phe Ala  
 210 215 220  
 Ala Gly Thr Ala Ala Ile Gln Pro Leu Asn Pro Glu Trp Asp Arg His  
 225 230 235  
 Leu Leu Asp Val Leu Ala Ser Gly Asp Leu Glu Gln Ile Asp Ala Trp  
 240 245 250 255  
 Thr Asn Asp Trp Phe Val Glu Gln Ala Gly His Ser Ser His Glu Val  
 260 265 270  
 Arg Thr Trp Ile Ala Ala Tyr Ala Ala Met Ser Ala Ala Gly Lys Tyr  
 275 280 285  
 Arg Val Thr Ser Thr Phe Tyr Arg Glu Ile His Glu Trp Ile Ala Gly  
 290 295 300  
 Phe Gly Ile Thr Thr Ala Val Ala Val Asp Glu  
 305 310 315

<210> 6  
 <211> 7599  
 <212> DNA  
 <213> Rhodococcus sp.

<220>  
 <221> CDS  
 <222> (4717)..(5586)  
 <223> ohpC hydrolase

<400> 000

|   |                         |      |
|---|-------------------------|------|
|   | atg acc cgt cct tac acc | 4734 |
|   | Met Thr Arg Pro Tyr Thr |      |
|   | 1 5                     |      |
| agc gtc tgg gac gac ctg aac cag gtc gag ttc agc cag gga ttc atc |                         | 4782 |
| Ser Val Trp Asp Asp Leu Asn Gln Val Glu Phe Ser Gln Gly Phe Ile |                         |      |
| 10 15 20  |                         |      |
| cag gcc ggc ccc tac cgg acc cga tac ctg cac gcc ggc gat tcg tcc |                         | 4830 |
| Gln Ala Gly Pro Tyr Arg Thr Arg Tyr Leu His Ala Gly Asp Ser Ser |                         |      |
| 25 30 35  |                         |      |
| aag ccc acg ctg atc ctg ctg cac ggc atc acc ggc cac gcc gag gcg |                         | 4878 |
| Lys Pro Thr Leu Ile Leu Leu His Gly Ile Thr Gly His Ala Glu Ala |                         |      |
| 40 45 50  |                         |      |



|   |      |
|---|------|
| tac gtg cgc aat ctg cgc tcg cat tcc gag cac ttc aac gtc tgg gca | 4926 |
| Tyr Val Arg Asn Leu Arg Ser His Ser Glu His Phe Asn Val Trp Ala |      |
| 55 60 65 70   |      |
| atc gac ttc atc ggc cac ggc tat tcg acc aag ccc gac cac ccg ctc | 4974 |
| Ile Asp Phe Ile Gly His Gly Tyr Ser Thr Lys Pro Asp His Pro Leu |      |
| 75 80 85  |      |
| gag atc aag cac tac atc gac cac gtg ctg cag ttg ctg gac gcc atc | 5022 |
| Glu Ile Lys His Tyr Ile Asp His Val Leu Gln Leu Leu Asp Ala Ile |      |
| 90 95 100   |      |
| ggc gtc gag aag gcc tcg ttt tcc ggg gag tct ctc ggc ggt tgg gtc | 5070 |
| Gly Val Glu Lys Ala Ser Phe Ser Gly Glu Ser Leu Gly Gly Trp Val |      |
| 105 110 115   |      |
| acc gcc cag ttc gcg cac gac cat ccc gag aag gtc gac cgg atc gtg | 5118 |
| Thr Ala Gln Phe Ala His Asp His Pro Glu Lys Val Asp Arg Ile Val |      |
| 120 125 130   |      |
| ctc aac acc atg ggc ggc acc atg gcc aac cct cag gtg atg gaa cgt | 5166 |
| Leu Asn Thr Met Gly Gly Thr Met Ala Asn Pro Gln Val Met Glu Arg |      |
| 135 140 145 150   |      |
| ctc tat acc ctg tcg atg gaa gcg gcg aag gac ccg agc tgg gaa cgc | 5214 |
| Leu Tyr Thr Leu Ser Met Glu Ala Ala Lys Asp Pro Ser Trp Glu Arg |      |
| 155 160 165   |      |
| gtc aaa gca cgc ctc gaa tgg ctc atg gcc gac ccg acc atg gtc acc | 5262 |
| Val Lys Ala Arg Leu Glu Trp Leu Met Ala Asp Pro Thr Met Val Thr |      |
| 170 175 180   |      |
| gac gac ctg atc cgc acc cgc cag gcc atc ttc cag cag ccg gat tgg | 5310 |
| Asp Asp Leu Ile Arg Thr Arg Gln Ala Ile Phe Gln Gln Pro Asp Trp |      |
| 185 190 195   |      |
| ctc aag gcc tgc gag atg aac atg gca ctg cag gac ctc gaa acc cgc | 5358 |
| Leu Lys Ala Cys Glu Met Asn Met Ala Leu Gln Asp Leu Glu Thr Arg |      |
| 200 205 210   |      |
| aag cgg aac atg atc acc gac gcc act ctc aac ggc atc acg gtg ccc | 5406 |
| Lys Arg Asn Met Ile Thr Asp Ala Thr Leu Asn Gly Ile Thr Val Pro |      |
| 215 220 225 230   |      |
| gcg atg gtg ctg tgg acc acc aag gac ccc tcc ggt ccg gtc gac gaa | 5454 |
| Ala Met Val Leu Trp Thr Thr Lys Asp Pro Ser Gly Pro Val Asp Glu |      |
| 235 240 245   |      |
| gcc aag cgc atc gcc tcc cac atc ccg ggc gcc aag ctg gcc atc atg | 5502 |
| Ala Lys Arg Ile Ala Ser His Ile Pro Gly Ala Lys Leu Ala Ile Met |      |
| 250 255 260   |      |
| gag aac tgt ggc cac tgg ccc cag tac gag gac ccc gag acc ttc aac | 5550 |
| Glu Asn Cys Gly His Trp Pro Gln Tyr Glu Asp Pro Glu Thr Phe Asn |      |
| 265 270 275   |      |

aag ctg cat ctg gac ttc ctc ctc ggt cgc agc tga  
 Lys Leu His Leu Asp Phe Leu Leu Gly Arg Ser  
 280 285 290

5596

<210> 7  
 <211> 289  
 <212> PRT  
 <213> Rhodococcus sp.

<400> 7

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Arg | Pro | Tyr | Thr | Ser | Val | Trp | Asp | Asp | Leu | Asn | Gln | Val | Glu | 1   | 5   | 10  | 15  |
| Phe | Ser | Gln | Gly | Phe | Ile | Gln | Ala | Gly | Pro | Tyr | Arg | Thr | Arg | Tyr | Leu | 20  | 25  | 30  |     |
| His | Ala | Gly | Asp | Ser | Ser | Lys | Pro | Thr | Leu | Ile | Leu | Leu | His | Gly | Ile | 35  | 40  | 45  |     |
| Thr | Gly | His | Ala | Glu | Ala | Tyr | Val | Arg | Asn | Leu | Arg | Ser | His | Ser | Glu | 50  | 55  | 60  |     |
| His | Phe | Asn | Val | Trp | Ala | Ile | Asp | Phe | Ile | Gly | His | Gly | Tyr | Ser | Thr | 65  | 70  | 75  | 80  |
| Lys | Pro | Asp | His | Pro | Leu | Glu | Ile | Lys | His | Tyr | Ile | Asp | His | Val | Leu | 85  | 90  | 95  |     |
| Gln | Leu | Leu | Asp | Ala | Ile | Gly | Val | Glu | Lys | Ala | Ser | Phe | Ser | Gly | Glu | 100 | 105 | 110 |     |
| Ser | Leu | Gly | Gly | Trp | Val | Thr | Ala | Gln | Phe | Ala | His | Asp | His | Pro | Glu | 115 | 120 | 125 |     |
| Lys | Val | Asp | Arg | Ile | Val | Leu | Asn | Thr | Met | Gly | Gly | Thr | Met | Ala | Asn | 130 | 135 | 140 |     |
| Pro | Gln | Val | Met | Glu | Arg | Leu | Tyr | Thr | Leu | Ser | Met | Glu | Ala | Ala | Lys | 145 | 150 | 155 | 160 |
| Asp | Pro | Ser | Trp | Glu | Arg | Val | Lys | Ala | Arg | Leu | Glu | Trp | Leu | Met | Ala | 165 | 170 | 175 |     |
| Asp | Pro | Thr | Met | Val | Thr | Asp | Asp | Leu | Ile | Arg | Thr | Arg | Gln | Ala | Ile | 180 | 185 | 190 |     |
| Phe | Gln | Gln | Pro | Asp | Trp | Leu | Lys | Ala | Cys | Glu | Met | Asn | Met | Ala | Leu | 195 | 200 | 205 |     |
| Gln | Asp | Leu | Glu | Thr | Arg | Lys | Arg | Asn | Met | Ile | Thr | Asp | Ala | Thr | Leu | 210 | 215 | 220 |     |
| Asn | Gly | Ile | Thr | Val | Pro | Ala | Met | Val | Leu | Trp | Thr | Thr | Lys | Asp | Pro | 225 | 230 | 235 | 240 |
| Ser | Gly | Pro | Val | Asp | Glu | Ala | Lys | Arg | Ile | Ala | Ser | His | Ile | Pro | Gly | 245 | 250 | 255 |     |
| Ala | Lys | Leu | Ala | Ile | Met | Glu | Asn | Cys | Gly | His | Trp | Pro | Gln | Tyr | Glu | 260 | 265 | 270 |     |
| Asp | Pro | Glu | Thr | Phe | Asn | Lys | Leu | His | Leu | Asp | Phe | Leu | Leu | Gly | Arg | 275 | 280 | 285 |     |
| Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 8  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial  
 Sequence:OHPR3  
  
 <400> 8  
 atcgaattcg gatccatgac caccacc 27  
  
 <210> 9  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial  
 Sequence:OHPR4  
  
 <400> 9  
 atcgcggccg ctctagacta actgcagggc gccaaagctcg gcag 44  
  
 <210> 10  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial  
 Sequence:C11  
  
 <400> 10  
 atcgaattcg gatccacgag agag 24  
  
 <210> 11  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial  
 Sequence:C12  
  
 <400> 11  
 atccggccgc gctctagagt acgcaagct 29  
  
 <210> 12  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial  
 Sequence:opl  
  
 <400> 12  
 atcctcgaga ccccgatacc 20

<210> 13  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial  
Sequence:op2

<400> 13  
atcgctcgacc gctaccc

17

<210> 14  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial  
Sequence:CaMVop2

<400> 14  
tccactgacg taagggatga cgcacaatcc cactatcctt cgcaagaccc

50

<210> 15  
<211> 99  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial  
Sequence:CaMVop3

<400> 15  
atgctagacg tctagttcag acgctactta tatagaggaa gggctcttgcg

50

<210> 16  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial  
Sequence:CaMVop4

<400> 16  
cgtctagcat tctagttgag gaagttcatt tcatttggag aggac

45

<210> 17  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial  
Sequence:CaMVopF1

<400> 17

atcgatatct ccactgacgt aag

23

<210> 18

<211> 24

<212> DNA

<213> Artificial Sequence :

<220>

<223> Description of Artificial  
Sequence:CaMVopR1

<400> 18

gatggatccg tcctctccaa atga

24

<210> 19

<211> 470

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimaeric  
promoter

<400> 19

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| catgcctgca  | ggtcaacatg | gtggagcacg | acactctcgt | ctactccaag | aatatcaaag | 60  |
| atacagtctc  | agaagaccag | agggctattg | agacttttca | acaaagggta | atatcgggaa | 120 |
| acctcctcgg  | attccattgc | ccagctatct | gtcacttcat | cgaaaggaca | gtagaaaagg | 180 |
| aagatgggctt | ctacaaatgc | catcattgcg | ataaaggaaa | ggctatcgtt | caagaatgcc | 240 |
| tctaccgaca  | gtggtcccaa | agatgtaccc | ccaccacga  | ggaacatcgt | ggaaaaagaa | 300 |
| gacgttccaa  | ccacgtcttc | aaagcaagtg | gattgatgtg | atatctccac | tgacgtaagg | 360 |
| gatgacgcac  | aatcccacta | tccttcgcaa | gacccttcct | ctatataagt | agcgtctgaa | 420 |
| ctagacgtct  | agcattctag | ttgaggaagt | tcatttcatt | tggagaggac |            | 470 |